

AMENDMENTS TO THE CLAIMS

1. (Original) A method for measuring a target nucleic acid comprising reacting said target nucleic acid, a labeled probe which is a labeled nucleic acid which hybridizes with said target nucleic acid, a non-labeled probe which is a nucleic acid having a nucleotide sequence complementary to a region in said target nucleic acid, which region is different from the region with which said labeled probe hybridizes, and an immobilized probe which is a nucleic acid bound to a support, which nucleic acid has a nucleotide sequence complementary to a region in said target nucleic acid, which region is different from the region with which said labeled probe hybridizes; and measuring the label of said labeled probe bound to said support; wherein an end region of said region with which said non-labeled probe hybridizes overlaps with an end region of said region with which said immobilized probe hybridizes.

2. (Original) The method according to claim 1, wherein the number of bases in the overlapping region is 1 to 5.

3. (Original) The method according to claim 2, wherein the number of bases in the overlapping region is 1 to 3.

4. (Original) The method according to any one of claims 1 to 3, wherein the region with which the 5'-end region of said non-labeled probe hybridizes and the region with which the 3'-end region of said immobilized probe hybridizes overlap.

5. (Currently Amended) The method according to ~~any one of claims 1 to 4~~ claim 1, wherein a mutant of said target nucleic acid exists, and the site of mutation is located within said region with which said immobilized probe hybridizes.
6. (Original) The method according to claim 5, wherein said site of mutation is located at a site apart from said overlapping region by 1 to 5 bases.
7. (Currently Amended) A method for detecting a single nucleotide polymorphism, comprising applying said method according to ~~any one of claims 1 to 6~~ claim 1 to a test sample containing said target nucleic acid or a mutant nucleic acid having a single nucleotide polymorphism of said target nucleic acid; and judging from the obtained measurement result whether the nucleic acid in said test sample is said target nucleic acid or said mutant nucleic acid.
8. (Currently Amended) A method for judging zygosity of a gene, comprising applying said method according to ~~any one of claims 1 to 6~~ claim 1 to a test sample containing a gene whose allele comprises a normal gene and an abnormal gene having a single nucleotide polymorphism; and judging from the obtained measurement result the zygosity of said gene.
9. (Currently Amended) A kit for measuring a nucleic acid, which is used for said method according to ~~any one of claims 1 to 6~~ claim 1, comprising at least said labeled probe, said non-labeled probe and said immobilized probe.